GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2004, 06:20:10 ; Search time 3182 Seconds
(without alignments)
131.386 Million cell updates/sec

Title: US-09-530-935-1
Perfect score: 14
Sequence: 1 tttgnnnnnnnncg 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	6	42.9	17	14	D11808	D11808 HUMHM01H11
	2	6	42.9	19	28	AZ769992	AZ769992 1M0571P12
c	3	6	42.9	20	28	AZ433830	AZ433830 1M0219I22
c	4	6	42.9	20	28	AZ628809	AZ628809 1M0481C17
c	5	6	42.9	22	28	AZ794014	AZ794014 2M0047O06
	6	6	42.9	22	28	AZ978258	AZ978258 2M0254O22
	7	6	42.9	23	28	AZ610143	AZ610143 1M0435H17
c	8	6	42.9	23	28	BH901489	BH901489 SALK_0796
c	9	6	42.9	23	28	BH901491	BH901491 SALK_0796
	10	6	42.9	24	9	AW064435	AW064435 SP1032 KR
c	11	6	42.9	24	13	BQ589506	BQ589506 E012561-0
c	12	6	42.9	24	29	TA306B12P	AL491238 T. brucei
	13	6	42.9	25	9	AI569102	AI569102 tr82b04.x
	14	6	42.9	25	9	AI697439	AI697439 tq08d09.x
	15	6	42.9	25	12	BM396446	BM396446 5009-0-20
	16	6	42.9	25	28	AZ372385	AZ372385 1M0124A16
	17	6	42.9	25	28	BH903608	BH903608 SALK_1030
	18	6	42.9	25	29	CG727695	CG727695 1119096A1
	19	6	42.9	26	12	BG899812	BG899812 HOA40-1-B
c	20	6	42.9	26	14	CF292605	CF292605 30DGS--01
c	21	6	42.9	26	28	AQ073689	AQ073689 EP(2)2563
	22	6	42.9	26	28	BH840727	BH840727 KG06970-3
	23	6	42.9	26	29	TA132H02P	AL465565 T. brucei
	24	6	42.9	26	29	TA194F01Q	AL477302 T. brucei
c	25	6	42.9	26	29	TA26H01P	AL453453 T. brucei
	26	6	42.9	27	28	BH850168	BH850168 SALK_0709
c	27	6	42.9	27	28	CC179962	CC179962 SALK_0745
	28	6	42.9	27	29	TA220E02Q	AL480330 T. brucei
c	29	6	42.9	28	9	AA868820	AA868820 ak54e05.s
c	30	6	42.9	28	9	AI358621	AI358621 qx20a04.x
c	31	6	42.9	28	9	AI434082	AI434082 ti41h03.x
	32	6	42.9	28	9	AI583841	AI583841 tt73e04.x
c	33	6	42.9	28	28	AQ025692	AQ025692 l(2)k0080
	34	6	42.9	28	28	AZ344267	AZ344267 1M0078L09
	35	6	42.9	28	28	AZ504358	AZ504358 1M0344F12
	36	6	42.9	28	28	BZ767739	BZ767739 SALK_1392
c	37	6	42.9	28	29	TA251H04P	AL483488 T. brucei
c	38	6	42.9	29	9	AU256240	AU256240 AU256240
	39	6	42.9	29	28	AZ360788	AZ360788 1M0104M12
c	40	6	42.9	29	28	AZ433903	AZ433903 1M0220G03
	41	6	42.9	29	28	AZ599962	AZ599962 1M0416N01
	42	6	42.9	29	28	AZ804312	AZ804312 2M0065D12
	43	6	42.9	29	28	BH011395	BH011395 BG01432-5
c	44	6	42.9	29	28	CC458567	CC458567 SALK_1197
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ALIGNMENTS

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LOCUS D11808 17 bp mRNA linear EST 02-DEC-1992
DEFINITION HUMHM01H11 Liver HepG2 cell line. Homo sapiens cDNA clone hm01h11, mRNA sequence.
ACCESSION D11808
VERSION D11808.1 GI:2155083
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Okubo,K., Hori,N., Matoba,R., Niiyama,T., Fukushima,A., Kojima,Y. and Matsubara,K.
TITLE Large scale cDNA sequencing for analysis of quantitative and qualitative aspects of gene expression
JOURNAL Nat. Genet. 2, 173-179 (1992)
MEDLINE 94258199
PUBMED 1345164
COMMENT Contact: Kousaku Okubo, Naohiro Hori, Ryo Matoba, Toshiyuki Niiyama, Atsushi Fukushima, Yuko Kojima & Kenichi Matsubara
Institute for Molecular and Cellular Biology
Osaka University
1-3 Yamada-oka,Suita,Osaka 565,Japan.
FEATURES Location/Qualifiers
source 1. .17

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:D0S8354E"
/db_xref="taxon:9606"
/clone="hm01h11"
/lab_host="E.coli"
/clone_lib="Liver HepG2 cell line."
/note="3'-directed regional cDNA library. Cleaved by MboI and transformed into E.coli."

ORIGIN

Query Match 42.9%; Score 6; DB 14; Length 17;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 TTTGNNNNNNNNCG 14
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Db         17 TTTGAGGTCGATCG 4
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RESULT 2
AZ769992
LOCUS AZ769992 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0571P12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0571P12 F, genomic survey sequence.
ACCESSION AZ769992
VERSION AZ769992.1 GI:12890713
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0571 row: P column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0571P12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.9%; Score 6; DB 28; Length 19;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db          1 TTTGAGTTTTCTCG 14
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RESULT 3
AZ433830/c
LOCUS AZ433830 20 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0219I22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0219I22 R, genomic survey sequence.
ACCESSION AZ433830
VERSION AZ433830.1 GI:10557843
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0219 row: I column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0219I22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.9%; Score 6; DB 28; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 TTTGNNNNNNNNCG 14
              ||||          ||
Db         17 TTTGTCATTTTTCG 4
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RESULT 4
AZ628809/c
LOCUS AZ628809 20 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0481C17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0481C17 F, genomic survey sequence.
ACCESSION AZ628809
VERSION AZ628809.1 GI:11750999
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0481 row: C column: 17
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0481C17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.9%; Score 6; DB 28; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 TTTGNNNNNNNNCG 14
              ||||          ||
Db         14 TTTGTGTGGGCGCG 1
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RESULT 5
AZ794014/c
LOCUS AZ794014 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0047O06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0047O06 R, genomic survey sequence.
ACCESSION AZ794014
VERSION AZ794014.1 GI:12939551
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0047 row: O column: 06
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0047O06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.9%; Score 6; DB 28; Length 22;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 TTTGNNNNNNNNCG 14
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Db         15 TTTGCCCAGTCACG 2
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RESULT 6
AZ978258
LOCUS AZ978258 22 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0254O22F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0254O22 F, genomic survey sequence.
ACCESSION AZ978258
VERSION AZ978258.1 GI:13849485
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0254 row: O column: 22
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0254O22"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.9%; Score 6; DB 28; Length 22;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 TTTGNNNNNNNNCG 14
              ||||          ||
Db          1 TTTGGAGTGTTCCG 14
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RESULT 7
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LOCUS AZ610143 23 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0435H17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0435H17 F, genomic survey sequence.
ACCESSION AZ610143
VERSION AZ610143.1 GI:11732333
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0435 row: H column: 17
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
FEATURES Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0435H17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.9%; Score 6; DB 28; Length 23;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db          9 TTTGGGCCGGGGCG 22
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RESULT 8
BH901489/c
LOCUS BH901489 23 bp DNA linear GSS 04-SEP-2002
DEFINITION SALK_079679.43.20.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_079679.43.20.x, genomic survey sequence.
ACCESSION BH901489
VERSION BH901489.1 GI:22712370
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 23)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of At5g50450.
Class: TDNA tagged.
FEATURES Location/Qualifiers
source 1. .23
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_079679.43.20.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 42.9%; Score 6; DB 28; Length 23;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         14 TTTGGCTAATGGCG 1
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RESULT 9
BH901491/c
LOCUS BH901491 23 bp DNA linear GSS 04-SEP-2002
DEFINITION SALK_079681.44.20.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_079681.44.20.x, genomic survey sequence.
ACCESSION BH901491
VERSION BH901491.1 GI:22712372
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 23)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of At5g50450.
Class: TDNA tagged.
FEATURES Location/Qualifiers
source 1. .23
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_079681.44.20.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 42.9%; Score 6; DB 28; Length 23;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         14 TTTGGCTAATGGCG 1
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RESULT 10
AW064435
LOCUS AW064435 24 bp mRNA linear EST 07-DEC-2000
DEFINITION SP1032 KRIBB Human CD4 intrathymic T-cell cDNA library Homo sapiens cDNA 3', mRNA sequence.
ACCESSION AW064435
VERSION AW064435.1 GI:8888372
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Goh,S.-H., Park,J.-H., Lee,Y.J., Lee,H.G., Yoo,H.-S., Lee,I.-C.,
            Park,J.-H., Kim,Y.-S. and Lee,C.-C.
  TITLE     Gene expression profile and identification of differentially
            expressed transcripts during human intrathymic T-cell development
            by cDNA sequencing analysis
  JOURNAL   Genomics 70 (1), 1-18 (2000)
  MEDLINE   20541704
   PUBMED   11087656
COMMENT     Contact: Sung-Ho Goh
            Genome Center
            Korea Research Institute of Bioscience and Biotechnology
            Oun-dong 52, Yu Sung-Gu, Daejon 305-333, Republic of Korea
            Tel: 82-42-860-4473
            Fax: 82-42-860-4479
            Email: gohsh@mail.kribb.re.kr
            Seq primer: T7
            High quality sequence stop: 24
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="Thymus"
                     /cell_type="Intrathymic T-cell"
                     /dev_stage="CD3+4+8- single positive stage"
                     /clone_lib="KRIBB Human CD4 intrathymic T-cell cDNA
                     library"
                     /note="Vector: pGEM-T; cDNA was made from total
                     cytoplasmic RNA of sorted human intrathymic CD3+4+8-
                     T-cell, adaptor ligated, amplified with PCR, and cloned
                     into pGEM-T vector."
ORIGIN

  Query Match             42.9%;  Score 6;  DB 9;  Length 24;
  Best Local Similarity   42.9%;  Pred. No. 1.4e+06;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         11 TTTGCCGTGGCTCG 24


RESULT 11
BQ589506/c
LOCUS       BQ589506                 24 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012561-024-015-I14-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-015-I14 5-PRIME, mRNA sequence.
ACCESSION   BQ589506
VERSION     BQ589506.1  GI:26119089
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 24   Std Error: 0.00
            Plate: 15  row: I  column: 14
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:187569"
                     /db_xref="taxon:161934"
                     /clone="024-015-I14"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN

  Query Match             42.9%;  Score 6;  DB 13;  Length 24;
  Best Local Similarity   42.9%;  Pred. No. 1.4e+06;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         20 TTTGGATTTTTGCG 7


RESULT 12
TA306B12P/c
LOCUS       TA306B12P                24 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 306b12, forward sequence,
            genomic survey sequence.
ACCESSION   AL491238
VERSION     AL491238.1  GI:11865450
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
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                     /db_xref="taxon:5691"
                     /clone="306b12"
ORIGIN

  Query Match             42.9%;  Score 6;  DB 29;  Length 24;
  Best Local Similarity   42.9%;  Pred. No. 1.4e+06;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         20 TTTGCCCTGTATCG 7


RESULT 13
AI569102
LOCUS       AI569102                 25 bp    mRNA    linear   EST 14-MAY-1999
DEFINITION  tr82b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224783 3'
            similar to TR:Q07611 Q07611 PROLINE-RICH PROTEOGLYCAN PRPG2. ;,
            mRNA sequence.
ACCESSION   AI569102
VERSION     AI569102.1  GI:4532476
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Life Technologies catalog #: 11548-013
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 1135   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1
            POLYA=No.
FEATURES              Location/Qualifiers
     source           1. .25
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2224783"
                      /tissue_type="adenocarcinoma"
                      /lab_host="DH10B"
                      /clone_lib="NCI_CGAP_Pan1"
                      /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.72 kb. Life Technologies catalog #:
                      11548-013"
ORIGIN

  Query Match             42.9%;  Score 6;  DB 9;  Length 25;
  Best Local Similarity   42.9%;  Pred. No. 1.5e+06;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db          1 TTTGGGGGGTCGCG 14


RESULT 14
AI697439
LOCUS       AI697439                 25 bp    mRNA    linear   EST 14-DEC-1999
DEFINITION  tq08d09.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2208209 3'
            similar to SW:RS5_HUMAN P46782 40S RIBOSOMAL PROTEIN S5. [1] ;,
            mRNA sequence.
ACCESSION   AI697439
VERSION     AI697439.1  GI:4985339
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 872   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
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                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2208209"
                      /tissue_type="poorly-differentiated endometrial
                      adenocarcinoma, 2 pooled tumors"
                      /lab_host="DH10B"
                      /clone_lib="NCI_CGAP_Ut3"
                      /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
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                      11541-018"
ORIGIN

  Query Match             42.9%;  Score 6;  DB 9;  Length 25;
  Best Local Similarity   42.9%;  Pred. No. 1.5e+06;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db          3 TTTGGCGCATACCG 16


RESULT 15
BM396446
LOCUS       BM396446                 25 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-20-G01.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM396446
VERSION     BM396446.1  GI:18196484
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
```

Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

```
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN

  Query Match             42.9%;  Score 6;  DB 12;  Length 25;
  Best Local Similarity   50.0%;  Pred. No. 1.5e+06;
  Matches    7;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||     |   ||
Db          9 TTTGGAGCNTCGCG 22


Search completed: April  5, 2004, 08:34:35
Job time : 3219 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2004, 07:39:24 ; Search time 332 Seconds
(without alignments)
157.719 Million cell updates/sec

Title: US-09-530-935-1
Perfect score: 14
Sequence: 1 tttgnnnnnnnncg 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2466186 seqs, 1870095128 residues

Total number of hits satisfying chosen parameters: 4932372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	6	42.9	15	9	US-09-504-231A-356	Sequence 356, App
c 2	6	42.9	15	9	US-09-274-553D-356	Sequence 356, App
c 3	6	42.9	15	14	US-10-104-473A-13	Sequence 13, Appl
c 4	6	42.9	15	15	US-10-440-850-204	Sequence 204, App
c 5	6	42.9	17	9	US-09-866-108-575	Sequence 575, App
c 6	6	42.9	17	9	US-09-866-108-576	Sequence 576, App
c 7	6	42.9	17	9	US-09-866-108-577	Sequence 577, App
c 8	6	42.9	17	9	US-09-866-108-578	Sequence 578, App
c 9	6	42.9	17	9	US-09-866-108-873	Sequence 873, App
c 10	6	42.9	17	9	US-09-866-108-874	Sequence 874, App
c 11	6	42.9	17	9	US-09-866-108-875	Sequence 875, App
c 12	6	42.9	17	9	US-09-866-108-876	Sequence 876, App
c 13	6	42.9	17	9	US-09-866-108-1095	Sequence 1095, Ap
c 14	6	42.9	17	9	US-09-866-108-1096	Sequence 1096, Ap
c 15	6	42.9	17	9	US-09-866-108-1097	Sequence 1097, Ap
c 16	6	42.9	17	9	US-09-866-108-1098	Sequence 1098, Ap
c 17	6	42.9	17	9	US-09-866-108-2678	Sequence 2678, Ap
c 18	6	42.9	17	9	US-09-866-108-2679	Sequence 2679, Ap
c 19	6	42.9	17	9	US-09-866-108-2680	Sequence 2680, Ap
c 20	6	42.9	17	9	US-09-866-108-2681	Sequence 2681, Ap
21	6	42.9	17	9	US-09-866-108-2821	Sequence 2821, Ap
22	6	42.9	17	9	US-09-866-108-2822	Sequence 2822, Ap
23	6	42.9	17	9	US-09-866-108-2823	Sequence 2823, Ap
24	6	42.9	17	9	US-09-866-108-2824	Sequence 2824, Ap
25	6	42.9	17	10	US-09-940-244-419	Sequence 419, App
c 26	6	42.9	17	10	US-09-730-289B-392	Sequence 392, App
c 27	6	42.9	17	10	US-09-730-289B-878	Sequence 878, App
c 28	6	42.9	17	10	US-09-818-875-1535	Sequence 1535, Ap
29	6	42.9	17	10	US-09-818-875-1536	Sequence 1536, Ap
30	6	42.9	17	10	US-09-818-875-2410	Sequence 2410, Ap
c 31	6	42.9	17	10	US-09-818-875-2411	Sequence 2411, Ap
32	6	42.9	17	10	US-09-818-875-2414	Sequence 2414, Ap
c 33	6	42.9	17	10	US-09-818-875-2415	Sequence 2415, Ap
34	6	42.9	17	10	US-09-818-875-2418	Sequence 2418, Ap
c 35	6	42.9	17	10	US-09-818-875-2419	Sequence 2419, Ap
36	6	42.9	17	10	US-09-818-875-2422	Sequence 2422, Ap
c 37	6	42.9	17	10	US-09-818-875-2423	Sequence 2423, Ap
38	6	42.9	17	10	US-09-877-478-257	Sequence 257, App
39	6	42.9	17	10	US-09-877-478-1705	Sequence 1705, Ap
40	6	42.9	17	10	US-09-877-478-2296	Sequence 2296, Ap
41	6	42.9	17	10	US-09-848-754A-892	Sequence 892, App
42	6	42.9	17	10	US-09-848-754A-893	Sequence 893, App
43	6	42.9	17	10	US-09-848-754A-3113	Sequence 3113, Ap
44	6	42.9	17	10	US-09-930-423-163	Sequence 163, App
45	6	42.9	17	10	US-09-930-423-1681	Sequence 1681, Ap

ALIGNMENTS

RESULT 1
US-09-504-231A-356/c
; Sequence 356, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 356
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-356

Query Match 42.9%; Score 6; DB 9; Length 15;
Best Local Similarity 42.9%; Pred. No. 2.1e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TTTGNNNNNNNNCG 14

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              ||||        ||
Db          15 TTTGCATGATGCCG 2


RESULT 2
US-09-274-553D-356/c
; Sequence 356, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
;  APPLICANT: Blatt, Lawrence
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Roberts, Beth
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Macejak, Dennis
;  TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
;  TITLE OF INVENTION:  HEPATITIS C VIRUS INFECTION
;  FILE REFERENCE: rpi 247/282
;  CURRENT APPLICATION NUMBER: US/09/274,553D
;  CURRENT FILING DATE:  1999-03-23
;  PRIOR APPLICATION NUMBER: 09/257,608
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/100,842
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/083,217
;  PRIOR FILING DATE: 1998-04-27
;  NUMBER OF SEQ ID NOS: 3148
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 356
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid Target
US-09-274-553D-356

  Query Match             42.9%;  Score 6;  DB 9;  Length 15;
  Best Local Similarity   42.9%;  Pred. No. 2.1e+05;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db          15 TTTGCATGATGCCG 2


RESULT 3
US-10-104-473A-13/c
; Sequence 13, Application US/10104473A
; Publication No. US20030165877A1
; GENERAL INFORMATION:
;  APPLICANT: Muyldermans, Serge
;  APPLICANT:  Silence, Karen
;  APPLICANT:  Steyaert, Jan
;  APPLICANT:  Torreele, Els
;  TITLE OF INVENTION: Recombinant Phages Capable of Entering
;  TITLE OF INVENTION:  Host Cells Via Specific Interaction with an Artificial
;  TITLE OF INVENTION:  Receptor
;  FILE REFERENCE: 11281-002002
;  CURRENT APPLICATION NUMBER: US/10/104,473A
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: PCT/EP00/09277
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: US 09/433,404
;  PRIOR FILING DATE: 1999-11-03
;  PRIOR APPLICATION NUMBER: EP 99402348.9
;  PRIOR FILING DATE: 1999-09-24
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-104-473A-13

  Query Match             42.9%;  Score 6;  DB 14;  Length 15;
  Best Local Similarity   42.9%;  Pred. No. 2.1e+05;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db          14 TTTGTCGGTGAACG 1


RESULT 4
US-10-440-850-204/c
; Sequence 204, Application US/10440850
; Publication No. US20030207837A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Jarvis, Thale
;  APPLICANT:  McSwiggen, Jim
;  TITLE CF INVENTION: Method and Reagent for the Induction of Graft Tolerance and Reve
;  TITLE CF INVENTION:  Immune Responses
;  FILE REFERENCE: 250/130 (MBHB00-900-A)
;  CURRENT APPLICATION NUMBER: US/10/440,850
;  CURRENT FILING DATE:  2003-05-19
;  PRIOR APPLICATION NUMBER: US/09/650,012
;  PRIOR FILING DATE: 2000-08-28
;  PRIOR APPLICATION NUMBER: US 08/585,684
;  PRIOR FILING DATE: 1996-01-12
;  PRIOR APPLICATION NUMBER: US 60/000,951
;  PRIOR FILING DATE: 1995-07-07
;  PRIOR APPLICATION NUMBER: US 09/038,073
;  PRIOR FILING DATE: 1998-03-11
;  NUMBER OF SEQ ID NOS: 2285
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 204
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-440-850-204

  Query Match             42.9%;  Score 6;  DB 15;  Length 15;
  Best Local Similarity   42.9%;  Pred. No. 2.1e+05;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db          15 TTTGACTGATAACG 2


RESULT 5
US-09-866-108-575/c
; Sequence 575, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 575
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-575

Query Match 42.9%; Score 6; DB 9; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
Qy          1 TTTGNNNNNNNNCG 14
              ||||         ||
Db         17 TTTGGTTGGTGTCG 4
```

RESULT 6
US-09-866-108-576/c
; Sequence 576, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 576
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-576

Query Match 42.9%; Score 6; DB 9; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 TTTGNNNNNNNNCG 14
              ||||         ||
Db         16 TTTGGTTGGTGTCG 3
```

RESULT 7
US-09-866-108-577/c
; Sequence 577, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 577
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-577

Query Match 42.9%; Score 6; DB 9; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TTTGNNNNNNNNCG 14
|||| ||
Db 15 TTTGGTTGGTGTCG 2

RESULT 8
US-09-866-108-578/c
; Sequence 578, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 578
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-578

Query Match 42.9%; Score 6; DB 9; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TTTGNNNNNNNNCG 14
|||| ||
Db 14 TTTGGTTGGTGTCG 1

RESULT 9
US-09-866-108-873/c
; Sequence 873, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 873
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-873

Query Match 42.9%; Score 6; DB 9; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TTTGNNNNNNNNCG 14
|||| ||
Db 17 TTTGACCCTCCTCG 4

```
RESULT 10
US-09-866-108-874/c
; Sequence 874, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 874
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-874

  Query Match             42.9%;  Score 6;  DB 9;  Length 17;
  Best Local Similarity   42.9%;  Pred. No. 2.1e+05;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||         ||
Db         16 TTTGACCCTCCTCG 3


RESULT 11
US-09-866-108-875/c
; Sequence 875, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 875
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-875

  Query Match             42.9%;  Score 6;  DB 9;  Length 17;
  Best Local Similarity   42.9%;  Pred. No. 2.1e+05;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||         ||
Db         15 TTTGACCCTCCTCG 2


RESULT 12
US-09-866-108-876/c
; Sequence 876, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
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; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 876
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-876

Query Match 42.9%; Score 6; DB 9; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         14 TTTGACCCTCCTCG 1
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RESULT 13
US-09-866-108-1095/c
; Sequence 1095, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1095
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1095

Query Match 42.9%; Score 6; DB 9; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         17 TTTGGGGCCTTACG 4
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RESULT 14
US-09-866-108-1096/c
; Sequence 1096, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1096
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1096

Query Match 42.9%; Score 6; DB 9; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         16 TTTGGGGCCTTACG 3
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RESULT 15
US-09-866-108-1097/c
; Sequence 1097, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1097
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1097

Query Match 42.9%; Score 6; DB 9; Length 17;
Best Local Similarity 42.9%; Pred. No. 2.1e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         15 TTTGGGGCCTTACG 2
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Search completed: April 5, 2004, 09:54:29
Job time : 364 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2004, 06:34:19 ; Search time 75 Seconds
(without alignments)
103.591 Million cell updates/sec

Title: US-09-530-935-1
Perfect score: 14
Sequence: 1 tttgnnnnnnnncg 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	6	42.9	15	1	US-08-182-968A-334	Sequence 334, App
c	2	6	42.9	15	2	US-08-774-306A-334	Sequence 334, App
c	3	6	42.9	15	2	US-08-585-684B-136	Sequence 136, App
c	4	6	42.9	15	2	US-08-963-946-11	Sequence 11, Appl
c	5	6	42.9	15	3	US-08-964-020-13	Sequence 13, Appl
c	6	6	42.9	15	3	US-09-064-156A-334	Sequence 334, App
c	7	6	42.9	15	3	US-09-038-073-136	Sequence 136, App
	8	6	42.9	16	4	US-09-371-772B-5851	Sequence 5851, Ap
	9	6	42.9	17	1	US-08-373-124A-1212	Sequence 1212, Ap
	10	6	42.9	17	1	US-08-435-628-1212	Sequence 1212, Ap
c	11	6	42.9	17	2	US-08-292-620A-1664	Sequence 1664, Ap
c	12	6	42.9	17	2	US-08-292-620A-1829	Sequence 1829, Ap
c	13	6	42.9	17	2	US-08-292-620A-1906	Sequence 1906, Ap
	14	6	42.9	17	3	US-08-988-706-32	Sequence 32, Appl
c	15	6	42.9	17	3	US-09-071-845-1664	Sequence 1664, Ap
c	16	6	42.9	17	3	US-09-071-845-1829	Sequence 1829, Ap
c	17	6	42.9	17	3	US-09-071-845-1906	Sequence 1906, Ap
	18	6	42.9	17	4	US-08-584-040-1996	Sequence 1996, Ap
	19	6	42.9	17	4	US-08-584-040-4222	Sequence 4222, Ap
c	20	6	42.9	17	4	US-08-584-040-5503	Sequence 5503, Ap
c	21	6	42.9	17	4	US-08-584-040-5504	Sequence 5504, Ap
	22	6	42.9	17	4	US-09-371-772B-541	Sequence 541, App
	23	6	42.9	17	4	US-09-371-772B-1989	Sequence 1989, Ap
c	24	6	42.9	17	4	US-09-371-772B-2394	Sequence 2394, Ap
c	25	6	42.9	17	4	US-09-371-772B-2395	Sequence 2395, Ap
	26	6	42.9	17	4	US-09-371-772B-4833	Sequence 4833, Ap
	27	6	42.9	17	4	US-09-371-772B-4834	Sequence 4834, Ap
c	28	6	42.9	17	4	US-09-371-772B-6364	Sequence 6364, Ap
c	29	6	42.9	17	4	US-09-371-772B-6365	Sequence 6365, Ap
	30	6	42.9	17	4	US-09-371-772B-6740	Sequence 6740, Ap
c	31	6	42.9	17	4	US-09-465-491-3	Sequence 3, Appli
c	32	6	42.9	17	4	US-09-866-108A-575	Sequence 575, App
c	33	6	42.9	17	4	US-09-866-108A-576	Sequence 576, App
c	34	6	42.9	17	4	US-09-866-108A-577	Sequence 577, App
c	35	6	42.9	17	4	US-09-866-108A-578	Sequence 578, App
c	36	6	42.9	17	4	US-09-866-108A-873	Sequence 873, App
c	37	6	42.9	17	4	US-09-866-108A-874	Sequence 874, App
c	38	6	42.9	17	4	US-09-866-108A-875	Sequence 875, App
c	39	6	42.9	17	4	US-09-866-108A-876	Sequence 876, App
c	40	6	42.9	17	4	US-09-866-108A-1095	Sequence 1095, Ap
c	41	6	42.9	17	4	US-09-866-108A-1096	Sequence 1096, Ap
c	42	6	42.9	17	4	US-09-866-108A-1097	Sequence 1097, Ap
c	43	6	42.9	17	4	US-09-866-108A-1098	Sequence 1098, Ap
c	44	6	42.9	17	4	US-09-866-108A-2678	Sequence 2678, Ap
c	45	6	42.9	17	4	US-09-866-108A-2679	Sequence 2679, Ap

ALIGNMENTS

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RESULT 1
US-08-182-968A-334/c
; Sequence 334, Application US/08182968A
; Patent No. 5610054
;  GENERAL INFORMATION:
;    APPLICANT:  Draper, Kenneth G.
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  INHIBITING HEPATITIS C
;    TITLE OF INVENTION:  VIRUS REPLICATION
;    NUMBER OF SEQUENCES:  497
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/182,968A
;      FILING DATE:  13-JANUARY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/882,888
;      FILING DATE:  14-MAY-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  205/277
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  334:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-182-968A-334

  Query Match            42.9%;  Score 6;  DB 1;  Length 15;
  Best Local Similarity  42.9%;  Pred. No. 2.1e+04;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;
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Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         15 TTTGCATGATGCCG 2


RESULT 2
US-08-774-306A-334/c
; Sequence 334, Application US/08774306A
; Patent No. 5869253
;  GENERAL INFORMATION:
;    APPLICANT:  Draper, Kenneth G.
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  INHIBITING HEPATITIS C
;    TITLE OF INVENTION:  VIRUS REPLICATION
;    NUMBER OF SEQUENCES:  497
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/774,306A
;      FILING DATE:  December 26, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/182,968
;      FILING DATE:  January 13, 1994
;      APPLICATION NUMBER:  07/882,888
;      FILING DATE:  May 14, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  223/227
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  334:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-774-306A-334

  Query Match             42.9%;  Score 6;  DB 2;  Length 15;
  Best Local Similarity   42.9%;  Pred. No. 2.1e+04;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         15 TTTGCATGATGCCG 2


RESULT 3
US-08-585-684B-136/c
; Sequence 136, Application US/08585684B
; Patent No. 5877021
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Daniel T.
;    APPLICANT:  Jarvis, Thale
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  INDUCTION OF GRAFT TOLERANCE
;    TITLE OF INVENTION:  AND REVERSAL OF IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  2751
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/585,684B
;      FILING DATE:  January 16, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/000,951
;      FILING DATE:  July 7, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/078
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  136:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-585-684B-136

  Query Match             42.9%;  Score 6;  DB 2;  Length 15;
  Best Local Similarity   42.9%;  Pred. No. 2.1e+04;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         15 TTTGACTGATAACG 2


RESULT 4
US-08-963-946-11/c
; Sequence 11, Application US/08963946
; Patent No. 5962273
;  GENERAL INFORMATION:
;    APPLICANT:  Durmowicz, Gerard P.
;    APPLICANT:  Harris, James M.
;    APPLICANT:  Yanson, Karen D.
;    TITLE OF INVENTION:  Detection of Neisseria Gonorrhoeae by
;    TITLE OF INVENTION:  Amplification and Detection of Its Nucleic Acid
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Richard J. Rodrick - Becton, Dickinson and
;      ADDRESSEE:  Company
;      STREET:  1 Becton Drive
;      CITY:  Franklin Lakes
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07417
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/963,946
;      FILING DATE:
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;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Highet, David W.
;       REGISTRATION NUMBER:  30,265
;       REFERENCE/DOCKET NUMBER:  P-3869
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (201) 847-5317
;       TELEFAX:  (201) 848-9228
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  15 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-963-946-11

  Query Match             42.9%;  Score 6;  DB 2;  Length 15;
  Best Local Similarity   42.9%;  Pred. No. 2.1e+04;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         14 TTTGATGATTTGCG 1


RESULT 5
US-08-964-020-13/c
; Sequence 13, Application US/08964020
; Patent No. 6077669
;  GENERAL INFORMATION:
;    APPLICANT:  Vonk, Glenn P.
;    APPLICANT:  Little, Michael C.
;    TITLE OF INVENTION:  Kit and Method for Fluorescence Based
;    TITLE OF INVENTION:  Detection Assay
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Richard J. Rodrick - Becton, Dickinson and
;      ADDRESSEE:  Company
;      STREET:  1 Becton Drive
;      CITY:  Franklin Lakes
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07417
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/964,020
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Highet, David W.
;      REGISTRATION NUMBER:  30,265
;      REFERENCE/DOCKET NUMBER:  p-4025
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 847-5317
;      TELEFAX:  (201) 848-9228
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-964-020-13

  Query Match             42.9%;  Score 6;  DB 3;  Length 15;
  Best Local Similarity   42.9%;  Pred. No. 2.1e+04;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         14 TTTGATGATTTGCG 1


RESULT 6
US-09-064-156A-334/c
; Sequence 334, Application US/09064156A
; Patent No. 6132966
;  GENERAL INFORMATION:
;    APPLICANT:  Draper, Kenneth G.
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  INHIBITING HEPATITIS C
;    TITLE OF INVENTION:  VIRUS REPLICATION
;    NUMBER OF SEQUENCES:  498
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/064,156A
;      FILING DATE:  April 21, 1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/774,306
;      FILING DATE:  December 26, 1996
;      APPLICATION NUMBER:  08/182,968
;      FILING DATE:  January 13, 1994
;      APPLICATION NUMBER:  07/882,888
;      FILING DATE:  May 14, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  234/083
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  334:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-064-156A-334

  Query Match             42.9%;  Score 6;  DB 3;  Length 15;
  Best Local Similarity   42.9%;  Pred. No. 2.1e+04;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         15 TTTGCATGATGCCG 2


RESULT 7
US-09-038-073-136/c
; Sequence 136, Application US/09038073
; Patent No. 6194150
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Daniel T.
;    APPLICANT:  Jarvis, Thale
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  INDUCTION OF GRAFT TOLERANCE
;    TITLE OF INVENTION:  AND REVERSAL OF IMMUNE RESPONSES
```

```
;    NUMBER OF SEQUENCES:  2751
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,073
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/585,684
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/078
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  136:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-038-073-136

  Query Match             42.9%;  Score 6;  DB 3;  Length 15;
  Best Local Similarity   42.9%;  Pred. No. 2.1e+04;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||         ||
Db         15 TTTGACTGATAACG 2


RESULT 8
US-09-371-772B-5851
; Sequence 5851, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5851
;   LENGTH: 16
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-5851

  Query Match             42.9%;  Score 6;  DB 4;  Length 16;
  Best Local Similarity   21.4%;  Pred. No. 2.1e+04;
  Matches    3;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              :::|         ||
Db          2 UUUGGCCUUGCCCG 15


RESULT 9
US-08-373-124A-1212
; Sequence 1212, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/373,124A
;      FILING DATE:  January 13, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1212:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-373-124A-1212

  Query Match             42.9%;  Score 6;  DB 1;  Length 17;
  Best Local Similarity   21.4%;  Pred. No. 2.1e+04;
  Matches    3;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              :::|         ||
Db          1 UUUGAGAUAUGACG 14
```

```
RESULT 10
US-08-435-628-1212
; Sequence 1212, Application US/08435628
; Patent No. 5817796
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,628
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/373,124
;      FILING DATE:  January 13, 1995
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1212:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-435-628-1212

  Query Match             42.9%;  Score 6;  DB 1;  Length 17;
  Best Local Similarity   21.4%;  Pred. No. 2.1e+04;
  Matches    3;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              :::|         ||
Db          1 UUUGAGAUAUGACG 14


RESULT 11
US-08-292-620A-1664/c
; Sequence 1664, Application US/08292620A
; Patent No. 5837542
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620A
;      FILING DATE:  August 17, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:                    two
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1664:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-292-620A-1664

  Query Match             42.9%;  Score 6;  DB 2;  Length 17;
  Best Local Similarity   42.9%;  Pred. No. 2.1e+04;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||         ||
Db         14 TTTGTGATCCTCCG 1


RESULT 12
US-08-292-620A-1829/c
; Sequence 1829, Application US/08292620A
; Patent No. 5837542
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
```

```
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620A
;      FILING DATE:  August 17, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:                    two
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1829:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-292-620A-1829

  Query Match             42.9%;  Score 6;  DB 2;  Length 17;
  Best Local Similarity   42.9%;  Pred. No. 2.1e+04;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||          ||
Db         14 TTTGTGATCCTCCG 1


RESULT 13
US-08-292-620A-1906/c
; Sequence 1906, Application US/08292620A
; Patent No. 5837542
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620A
;      FILING DATE:  August 17, 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:                    two
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1906:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-292-620A-1906

  Query Match             42.9%;  Score 6;  DB 2;  Length 17;
  Best Local Similarity   42.9%;  Pred. No. 2.1e+04;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||          ||
Db         14 TTTGTGATCCTCCG 1


RESULT 14
US-08-988-706-32
; Sequence 32, Application US/08988706
; Patent No. 6083698
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, Sheri J.
;    APPLICANT:  ANGELLY, Tracy S.
;    APPLICANT:  LAWRENCE, Tammy
;    APPLICANT:  LESCALLETT, Jennifer L.
;    APPLICANT:  MURPHY, Patricia D.
;    APPLICANT:  ALLEN, Antonette P.
;    APPLICANT:  THRUBER, Denise B.
;    APPLICANT:  WHITE, Marga B.
;    APPLICANT:  ZENG, Bin
;    APPLICANT:  SADZEWICZ, Lisa K.
;    TITLE OF INVENTION:  CANCER SUSCEPTIBILITY MUTATIONS OF BRCA1
;    NUMBER OF SEQUENCES:  55
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oncormed, Inc.
;      STREET:  205 Perry Parkway
;      CITY:  Gaithersburg
;      STATE:  MD
;      COUNTRY:  USA
;      ZIP:  20877
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/988,706
;       FILING DATE:
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  TARCZA, John E.
;       REGISTRATION NUMBER:  33,638
;       REFERENCE/DOCKET NUMBER:  PA-0108
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  301-208-1888
;       TELEFAX:  301-926-6125
;   INFORMATION FOR SEQ ID NO:  32:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  17 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "PROBE"
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FRAGMENT TYPE:  internal
;     ORIGINAL SOURCE:
;       ORGANISM:  HOMO SAPIENS
;       STRAIN:  BRCA1
US-08-988-706-32

  Query Match             42.9%;  Score 6;  DB 3;  Length 17;
  Best Local Similarity   42.9%;  Pred. No. 2.1e+04;
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Db          2 TTTGTGTGTGAACG 15


RESULT 15
US-09-071-845-1664/c
; Sequence 1664, Application US/09071845
; Patent No. 6132967
;  GENERAL INFORMATION:
;    APPLICANT:  Susan Grimm
;    APPLICANT:  Dan T. Stinchcomb
;    APPLICANT:  James McSwiggen
;    APPLICANT:  Sean Sullivan
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  INTRACELLULAR ADHESION
;    TITLE OF INVENTION:  MOLECULE-1 (I-CAM-1)
;    NUMBER OF SEQUENCES:  2390
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,845
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/292,620
;      FILING DATE:  August 17, 1994
;      APPLICATION NUMBER:  08/008,895
;      FILING DATE:  January 19, 1993
;      APPLICATION NUMBER:  07/989,849
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1664:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-071-845-1664

  Query Match             42.9%;  Score 6;  DB 3;  Length 17;
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  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
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Db         14 TTTGTGATCCTCCG 1


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Job time : 85 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2004, 04:01:04 ; Search time 2915 Seconds
(without alignments)
208.166 Million cell updates/sec

Title: US-09-530-935-1
Perfect score: 14
Sequence: 1 tttgnnnnnnnncg 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6	42.9	14	6	BD135830	BD135830 Selective
2	6	42.9	14	6	BD135832	BD135832 Selective
3	6	42.9	14	6	BD135833	BD135833 Selective
4	6	42.9	14	6	BD135836	BD135836 Selective
5	6	42.9	14	6	BD135837	BD135837 Selective
c 6	6	42.9	15	6	AR033568	AR033568 Sequence
c 7	6	42.9	15	6	AR078071	AR078071 Sequence
c 8	6	42.9	15	6	AR098738	AR098738 Sequence
c 9	6	42.9	15	6	AR113390	AR113390 Sequence
c 10	6	42.9	15	6	AR131711	AR131711 Sequence
c 11	6	42.9	15	6	E35652	E35652 Detection o
c 12	6	42.9	15	6	E35697	E35697 Detection a
c 13	6	42.9	15	6	I57797	I57797 Sequence 33
c 14	6	42.9	15	6	AX100916	AX100916 Sequence
c 15	6	42.9	15	6	BD005865	BD005865 Novel pro
16	6	42.9	15	6	BD135831	BD135831 Selective
c 17	6	42.9	15	6	BD207301	BD207301 Enzymatic
18	6	42.9	16	6	AR328449	AR328449 Sequence
19	6	42.9	16	6	AX132920	AX132920 Sequence
c 20	6	42.9	17	6	A05414	A05414 Synthetic o
c 21	6	42.9	17	6	A09621	A09621 Oligonucleo
22	6	42.9	17	6	AR046419	AR046419 Sequence
c 23	6	42.9	17	6	AR057460	AR057460 Sequence
c 24	6	42.9	17	6	AR057625	AR057625 Sequence
c 25	6	42.9	17	6	AR057702	AR057702 Sequence
26	6	42.9	17	6	AR101677	AR101677 Sequence
c 27	6	42.9	17	6	AR115218	AR115218 Sequence
c 28	6	42.9	17	6	AR115383	AR115383 Sequence
c 29	6	42.9	17	6	AR115460	AR115460 Sequence
c 30	6	42.9	17	6	BD235248	BD235248 Presenili
c 31	6	42.9	17	6	BD240764	BD240764 Method fo
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c 35	6	42.9	17	6	AR190015	AR190015 Sequence
c 36	6	42.9	17	6	AR190016	AR190016 Sequence
37	6	42.9	17	6	AR323139	AR323139 Sequence
38	6	42.9	17	6	AR324587	AR324587 Sequence
c 39	6	42.9	17	6	AR324992	AR324992 Sequence
c 40	6	42.9	17	6	AR324993	AR324993 Sequence
41	6	42.9	17	6	AR327431	AR327431 Sequence
42	6	42.9	17	6	AR327432	AR327432 Sequence
c 43	6	42.9	17	6	AR328962	AR328962 Sequence
c 44	6	42.9	17	6	AR328963	AR328963 Sequence
45	6	42.9	17	6	AR329338	AR329338 Sequence

ALIGNMENTS

RESULT 1
BD135830
LOCUS BD135830 14 bp DNA linear PAT 18-SEP-2002
DEFINITION Selective regulation of adenovirus production.
ACCESSION BD135830
VERSION BD135830.1 GI:23230775
KEYWORDS JP 2002506355-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Hearing,P., Schmid,S.I., Ostapchuk,P.H. and Erturk,E.
TITLE Selective regulation of adenovirus production
JOURNAL Patent: JP 2002506355-A 1 26-FEB-2002;
THE RESEARCH FOUNDATION OF STATE UNIVERSITY OF NEW YORK

```
COMMENT     OS   Artificial Sequence
            PN   JP 2002506355-A/1
            PD   26-FEB-2002
            PF   15-APR-1999 JP 1999552110
            PR   15-APR-1998 US    60/081867,05-JUN-1998 US    60/088321 PI
            PATRICK HEARING,SUSANNE I SCHMID,PHILONIENA H OSTAPCHUK,ECE  PI
            ERTURK
            PC   C12N15/86
            CC   Selective regulation of adenovirus production FH   Key
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Db          1 TTTGNNNNNNNNCG 14


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DEFINITION  Selective regulation of adenovirus production.
ACCESSION   BD135832
VERSION     BD135832.1  GI:23230777
KEYWORDS    JP 2002506355-A/3.
SOURCE      unidentified adenovirus
  ORGANISM  unidentified adenovirus
            Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Hearing,P., Schmid,S.I., Ostapchuk,P.H. and Erturk,E.
  TITLE     Selective regulation of adenovirus production
  JOURNAL   Patent: JP 2002506355-A 3 26-FEB-2002;
            THE RESEARCH FOUNDATION OF STATE UNIVERSITY OF NEW YORK
COMMENT     OS   Adenovirus
            PN   JP 2002506355-A/3
            PD   26-FEB-2002
            PF   15-APR-1999 JP 1999552110
            PR   15-APR-1998 US    60/081867,05-JUN-1998 US    60/088321 PI
            PATRICK HEARING,SUSANNE I SCHMID,PHILONIENA H OSTAPCHUK,ECE  PI
            ERTURK
            PC   C12N15/86
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Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db          1 TTTGGGCGTAACCG 14


RESULT 3
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LOCUS       BD135833                  14 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Selective regulation of adenovirus production.
ACCESSION   BD135833
VERSION     BD135833.1  GI:23230778
KEYWORDS    JP 2002506355-A/4.
SOURCE      unidentified adenovirus
  ORGANISM  unidentified adenovirus
            Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Hearing,P., Schmid,S.I., Ostapchuk,P.H. and Erturk,E.
  TITLE     Selective regulation of adenovirus production
  JOURNAL   Patent: JP 2002506355-A 4 26-FEB-2002;
            THE RESEARCH FOUNDATION OF STATE UNIVERSITY OF NEW YORK
COMMENT     OS   Adenovirus
            PN   JP 2002506355-A/4
            PD   26-FEB-2002
            PF   15-APR-1999 JP 1999552110
            PR   15-APR-1998 US    60/081867,05-JUN-1998 US    60/088321 PI
            PATRICK HEARING,SUSANNE I SCHMID,PHILONIENA H OSTAPCHUK,ECE  PI
            ERTURK
            PC   C12N15/86
            CC   AII
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Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
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LOCUS       BD135836                  14 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Selective regulation of adenovirus production.
ACCESSION   BD135836
VERSION     BD135836.1  GI:23230781
KEYWORDS    JP 2002506355-A/7.
SOURCE      unidentified adenovirus
  ORGANISM  unidentified adenovirus
            Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Hearing,P., Schmid,S.I., Ostapchuk,P.H. and Erturk,E.
  TITLE     Selective regulation of adenovirus production
  JOURNAL   Patent: JP 2002506355-A 7 26-FEB-2002;
            THE RESEARCH FOUNDATION OF STATE UNIVERSITY OF NEW YORK
COMMENT     OS   Adenovirus
            PN   JP 2002506355-A/7
            PD   26-FEB-2002
            PF   15-APR-1999 JP 1999552110
            PR   15-APR-1998 US    60/081867,05-JUN-1998 US    60/088321 PI
            PATRICK HEARING,SUSANNE I SCHMID,PHILONIENA H OSTAPCHUK,ECE  PI
            ERTURK
            PC   C12N15/86
            CC   AV
            FH   Key             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   42.9%;  Pred. No. 1.8e+06;
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Qy          1 TTTGNNNNNNNNCG 14
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Db          1 TTTGTCTAGGGCCG 14


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LOCUS       BD135837                 14 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Selective regulation of adenovirus production.
ACCESSION   BD135837
VERSION     BD135837.1  GI:23230782
KEYWORDS    JP 2002506355-A/8.
SOURCE      unidentified adenovirus
  ORGANISM  unidentified adenovirus
            Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Hearing,P., Schmid,S.I., Ostapchuk,P.H. and Erturk,E.
  TITLE     Selective regulation of adenovirus production
  JOURNAL   Patent: JP 2002506355-A 8 26-FEB-2002;
            THE RESEARCH FOUNDATION OF STATE UNIVERSITY OF NEW YORK
COMMENT     OS   Adenovirus
            PN   JP 2002506355-A/8
            PD   26-FEB-2002
            PF   15-APR-1999 JP 1999552110
            PR   15-APR-1998 US    60/081867,05-JUN-1998 US    60/088321 PI
            PATRICK HEARING,SUSANNE I SCHMID,PHILONIENA H OSTAPCHUK,ECE  PI
            ERTURK
            PC   C12N15/86
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RESULT 6
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DEFINITION  Sequence 334 from patent US 5869253.
ACCESSION   AR033568
VERSION     AR033568.1  GI:5949173
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting hepatitis C virus replication
  JOURNAL   Patent: US 5869253-A 334 09-FEB-1999;
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ORIGIN

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Db         15 TTTGCATGATGCCG 2


RESULT 7
AR078071/c
LOCUS       AR078071                 15 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 11 from patent US 5962273.
ACCESSION   AR078071
VERSION     AR078071.1  GI:10004817
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Durmowicz,G.P., Harris,J.M. and Yanson,K.Dilly.
  TITLE     Detection of Neisseria gonorrhoeae by amplification and detection
            of its nucleic acid
  JOURNAL   Patent: US 5962273-A 11 05-OCT-1999;
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LOCUS       AR098738                 15 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 13 from patent US 6077669.
ACCESSION   AR098738
VERSION     AR098738.1  GI:12808504
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Little,M.C. and Vonk,G.P.
  TITLE     Kit and method for fluorescence based detection assay
  JOURNAL   Patent: US 6077669-A 13 20-JUN-2000;
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Qy          1 TTTGNNNNNNNNCG 14
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RESULT 9
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DEFINITION  Sequence 334 from patent US 6132966.
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ACCESSION   AR113390
VERSION     AR113390.1  GI:14093712
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting hepatitis C virus replication
  JOURNAL   Patent: US 6132966-A 334 17-OCT-2000;
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LOCUS       AR131711                  15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 136 from patent US 6194150.
ACCESSION   AR131711
VERSION     AR131711.1  GI:14120614
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
  TITLE     Nucleic acid based inhibition of CD40
  JOURNAL   Patent: US 6194150-A 136 27-FEB-2001;
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RESULT 11
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LOCUS       E35652                    15 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Detection of Neisseria gonorrhoeae by amplifying and detecting
            nucleic acid of Neisseria gonorrhoeae.
ACCESSION   E35652
VERSION     E35652.1  GI:13019128
KEYWORDS    JP 1999225781-A/11.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Jerrold,B.D., James,M.H. and Karen,D.Y.
  TITLE     Detection of Neisseria gonorrhoeae by amplifying and detecting
            nucleic acid of Neisseria gonorrhoeae
  JOURNAL   Patent: JP 1999225781-A 11 24-AUG-1999;
            BECTON DICKINSON & CO
COMMENT     OS   Artifical Sequence
            PN   JP 1999225781-A/11
            PD   24-AUG-1999
            PF   30-OCT-1998 JP 1998309591
            PR   04-NOV-1997 US    08/963946
            PI   JERROLD B DAMOWITSU,JAMES M HARRIS,KAREN DIRI YANSON PC
            C12N15/09,C12M1/00,C12Q1/68//G01N33/571,(C12N15/09,C12R1:36), PC
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FEATURES             Location/Qualifiers
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                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match           42.9%;  Score 6;  DB 6;  Length 15;
  Best Local Similarity   42.9%;  Pred. No. 1.8e+06;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         14 TTTGATGATTTGCG 1


RESULT 12
E35697/c
LOCUS       E35697                    15 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Detection assay with the use of fluorescence and kit therefor.
ACCESSION   E35697
VERSION     E35697.1  GI:13019169
KEYWORDS    JP 1999225799-A/13.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Michael,C.L. and Gren,P.V.
  TITLE     Detection assay with the use of fluorescence and kit therefor
  JOURNAL   Patent: JP 1999225799-A 13 24-AUG-1999;
            BECTON DICKINSON & CO
COMMENT     OS   Artificial Sequence
            PN   JP 1999225799-A/13
            PD   24-AUG-1999
            PF   04-NOV-1998 JP 1998312790
            PR   04-NOV-1997 US    08/964020
            PI   MICHAEL C LITTLE,GREN P VONG
            PC   C12Q1/68,G01N21/78,G01N33/50//C12N15/09,C12N15/00 CC
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .15
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                     /db_xref="taxon:32630"
ORIGIN

  Query Match           42.9%;  Score 6;  DB 6;  Length 15;
  Best Local Similarity   42.9%;  Pred. No. 1.8e+06;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         14 TTTGATGATTTGCG 1


RESULT 13
I57797/c
LOCUS       I57797                    15 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 334 from patent US 5610054.
ACCESSION   I57797
VERSION     I57797.1  GI:2482861
KEYWORDS    .
```

```
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Draper,K.G.
  TITLE     Enzymatic RNA molecule targeted against Hepatitis C virus
  JOURNAL   Patent: US 5610054-A 334 11-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             42.9%;  Score 6;  DB 6;  Length 15;
  Best Local Similarity   42.9%;  Pred. No. 1.8e+06;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         15 TTTGCATGATGCCG 2


RESULT 14
AX100916/c
LOCUS       AX100916                  15 bp    DNA     linear   PAT 10-APR-2001
DEFINITION  Sequence 13 from Patent WO0121817.
ACCESSION   AX100916
VERSION     AX100916.1  GI:13619808
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Muyldermans,S., Silence,K., Steyaert,J. and Toreele,E.
  TITLE     Recombinant phages capable of entering host cells via specific
            interaction with an artificial receptor
  JOURNAL   Patent: WO 0121817-A 13 29-MAR-2001;
            Vlaams Interuniversitair Instituut voor Biotechnologie vz; w. (BE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
     misc_feature    1. .15
                     /note="primer"
ORIGIN

  Query Match             42.9%;  Score 6;  DB 6;  Length 15;
  Best Local Similarity   42.9%;  Pred. No. 1.8e+06;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         14 TTTGTCGGTGAACG 1


RESULT 15
BD005865/c
LOCUS       BD005865                  15 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Novel probes for the detection of Mycobacteria.
ACCESSION   BD005865
VERSION     BD005865.1  GI:18634236
KEYWORDS    JP 2001501825-A/76.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stender,H., Lund,K. and Mollerup,T.A.
  TITLE     Novel probes for the detection of Mycobacteria
  JOURNAL   Patent: JP 2001501825-A 76 13-FEB-2001;
            DAKO AS
COMMENT     OS   Unidentified
            PN   JP 2001501825-A/76
            PD   13-FEB-2001
            PF   03-OCT-1997 JP 1998517095
            PR   04-OCT-1996 DK      1096/96,18-OCT-1996 DK      1156/96 PR
            05-MAY-1997 DK      0512/97
            PI   HENRIK STENDER,KAARE LUND,TINA ANDRESEN MOLLERUP PC
            C12Q1/68,C07K14/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             42.9%;  Score 6;  DB 6;  Length 15;
  Best Local Similarity   42.9%;  Pred. No. 1.8e+06;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         14 TTTGTGTGGAGTCG 1


Search completed: April  5, 2004, 07:39:16
Job time : 2919 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2004, 03:57:00 ; Search time 398 Seconds
(without alignments)
149.434 Million cell updates/sec

Title: US-09-530-935-1
Perfect score: 14
Sequence: 1 tttgnnnnnnnncg 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	6	42.9	14	3	AAZ59890	Aaz59890 Adenoviru
	2	6	42.9	14	3	AAZ59894	Aaz59894 Adenoviru
	3	6	42.9	14	3	AAZ59895	Aaz59895 Adenoviru
	4	6	42.9	14	3	AAZ59891	Aaz59891 Adenoviru
c	5	6	42.9	15	2	AAX64642	Aax64642 Human B7-
c	6	6	42.9	15	2	AAX56323	Aax56323 Neisseria
c	7	6	42.9	15	2	AAX30272	Aax30272 Neisseria
c	8	6	42.9	15	3	AAZ62723	Aaz62723 Substrate
	9	6	42.9	15	3	AAZ59897	Aaz59897 Consensus
c	10	6	42.9	15	4	AAF46301	Aaf46301 IGFBP2 ol
	11	6	42.9	15	4	AAF52545	Aaf52545 IGF-I oli
c	12	6	42.9	15	4	AAF47804	Aaf47804 IGFBP3 ol
	13	6	42.9	15	4	AAF49895	Aaf49895 IGF-I oli
	14	6	42.9	15	4	AAF52544	Aaf52544 IGF-I oli
	15	6	42.9	15	4	AAF52808	Aaf52808 IGF-I oli
c	16	6	42.9	15	4	AAF46300	Aaf46300 IGFBP2 ol
	17	6	42.9	15	4	AAF52809	Aaf52809 IGF-I oli
c	18	6	42.9	15	4	AAF47805	Aaf47805 IGFBP3 ol
	19	6	42.9	15	4	AAF49896	Aaf49896 IGF-I oli
c	20	6	42.9	15	4	AAF57499	Aaf57499 pBAD-Oprl
c	21	6	42.9	15	6	ABN81405	Abn81405 Human HTA
	22	6	42.9	15	6	AAD43773	Aad43773 Human AGT
c	23	6	42.9	15	6	ABX00574	Abx00574 Hepatitis
c	24	6	42.9	15	7	ABX76550	Abx76550 M. avium
c	25	6	42.9	16	2	AAQ21918	Aaq21918 TEG-termi
	26	6	42.9	16	2	AAT91222	Aat91222 Hairpin r
	27	6	42.9	16	3	AAA86548	Aaa86548 Cyclin B1
	28	6	42.9	16	5	AAH61714	Aah61714 Cyclin B1
c	29	6	42.9	17	2	AAT53489	Aat53489 Rat ICAM
c	30	6	42.9	17	2	AAT53639	Aat53639 Rat ICAM
c	31	6	42.9	17	2	AAT53696	Aat53696 Rat ICAM
	32	6	42.9	17	2	AAT81651	Aat81651 Human c-m
	33	6	42.9	17	2	AAX71472	Aax71472 Human KDR
c	34	6	42.9	17	2	AAX72753	Aax72753 Mouse flk
	35	6	42.9	17	2	AAX69246	Aax69246 Human flt
c	36	6	42.9	17	2	AAX72754	Aax72754 Mouse flk
	37	6	42.9	17	2	AAV96670	Aav96670 Potato ci
	38	6	42.9	17	2	AAA18878	Aaa18878 Human TIE
c	39	6	42.9	17	2	AAV93663	Aav93663 Human B-r
	40	6	42.9	17	2	AAV90956	Aav90956 Human C-r
c	41	6	42.9	17	2	AAV92584	Aav92584 Human A-R
	42	6	42.9	17	2	AAX80251	Aax80251 Human BRC
c	43	6	42.9	17	3	AAZ45960	Aaz45960 Human pre
	44	6	42.9	17	3	AAZ56918	Aaz56918 MMCP-4 ge
c	45	6	42.9	17	3	AAA80154	Aaa80154 Hepatitis

ALIGNMENTS

RESULT 1
AAZ59890
ID AAZ59890 standard; DNA; 14 BP.
XX
AC AAZ59890;
XX
DT 08-MAY-2000 (first entry)
XX
DE Adenovirus minimal packaging element, A repeat AI.
XX
KW Adenovirus; minimal packaging element; A repeat; repressor binding site;
KW DNA delivery; ds.
XX
OS Mastadenovirus.
XX
PN WO9953085-A2.
XX
PD 21-OCT-1999.
XX
PF 15-APR-1999; 99WO-US008294.
XX
PR 15-APR-1998; 98US-0081867P.
PR 05-JUN-1998; 98US-0088321P.
XX
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
XX
PI Hearing P, Schmid SI, Ostapchuk PH, Erturk E;
XX
DR WPI; 2000-052657/04.
XX
PT Regulating adenoviral packaging by incorporation of repressor binding
PT sites that allow selective suppression of packaging, used for gene
PT therapy.
XX
PS Disclosure; Page 15; 71pp; English.
XX
CC The invention relates to the regulation of adenoviral packaging. The
CC method of the invention comprises propagating an adenoviral vector
CC containing a repressor binding site, in the absence of the repressor.
CC After propagation, vector packaging is repressed by the appropriate
CC repressor protein. The invention also encompasses an adenoviral vector
CC that includes an adenoviral packaging sequence containing several COUP-TF
CC (chicken ovalbumin upstream promoter transcription factor) binding sites
CC (AAZ59919). Adenoviral vectors containing repressor binding sites are
CC used for DNA delivery, e.g., for expression of a therapeutic protein; in
CC genetic immunisation; or to produce antiviral DNA or antisense RNA.

CC Typical heterologous genes that can be expressed include those for
CC interleukin-2, alpha1-antitrypsin, cystic fibrosis transmembrane
CC conductance regulator and coagulation factor VIII. These vectors have
CC very large capacity (up to 36 kb) for foreign DNA and minimise the risk
CC of generating replication competent virus (since vector and helper virus
CC can be designed such that they have no overlapping packaging sequences
CC that might permit homologous recombination). The presence of the
CC repressor binding site allows selective inhibition of virion production
CC (i.e., packaging of one vector in presence of another). Sequences
CC AAZ59890-Z59896 represent adenovirus minimal packaging elements,
CC designated A repeats AI-AVII, and AAZ59897 represents a consensus of
CC these A repeats
XX
SQ Sequence 14 BP; 2 A; 3 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 42.9%; Score 6; DB 3; Length 14;
Best Local Similarity 42.9%; Pred. No. 2e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TTTGNNNNNNNNCG 14
|||| ||
Db 1 TTTGGGCGTAACCG 14

RESULT 2
AAZ59894
ID AAZ59894 standard; DNA; 14 BP.
XX
AC AAZ59894;
XX
DT 08-MAY-2000 (first entry)
XX
DE Adenovirus minimal packaging element, A repeat AV.
XX
KW Adenovirus; minimal packaging element; A repeat; repressor binding site;
KW DNA delivery; ds.
XX
OS Mastadenovirus.
XX
PN WO9953085-A2.
XX
PD 21-OCT-1999.
XX
PF 15-APR-1999; 99WO-US008294.
XX
PR 15-APR-1998; 98US-0081867P.
PR 05-JUN-1998; 98US-0088321P.
XX
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
XX
PI Hearing P, Schmid SI, Ostapchuk PH, Erturk E;
XX
DR WPI; 2000-052657/04.
XX
PT Regulating adenoviral packaging by incorporation of repressor binding
PT sites that allow selective suppression of packaging, used for gene
PT therapy.
XX
PS Disclosure; Page 15; 71pp; English.
XX
CC The invention relates to the regulation of adenoviral packaging. The
CC method of the invention comprises propagating an adenoviral vector
CC containing a repressor binding site, in the absence of the repressor.
CC After propagation, vector packaging is repressed by the appropriate
CC repressor protein. The invention also encompasses an adenoviral vector
CC that includes an adenoviral packaging sequence containing several COUP-TF
CC (chicken ovalbumin upstream promoter transcription factor) binding sites
CC (AAZ59919). Adenoviral vectors containing repressor binding sites are
CC used for DNA delivery, e.g., for expression of a therapeutic protein; in
CC genetic immunisation; or to produce antiviral DNA or antisense RNA.
CC Typical heterologous genes that can be expressed include those for
CC interleukin-2, alpha1-antitrypsin, cystic fibrosis transmembrane
CC conductance regulator and coagulation factor VIII. These vectors have
CC very large capacity (up to 36 kb) for foreign DNA and minimise the risk
CC of generating replication competent virus (since vector and helper virus
CC can be designed such that they have no overlapping packaging sequences
CC that might permit homologous recombination). The presence of the
CC repressor binding site allows selective inhibition of virion production
CC (i.e., packaging of one vector in presence of another). Sequences
CC AAZ59890-Z59896 represent adenovirus minimal packaging elements,
CC designated A repeats AI-AVII, and AAZ59897 represents a consensus of
CC these A repeats
XX
SQ Sequence 14 BP; 1 A; 3 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 42.9%; Score 6; DB 3; Length 14;
Best Local Similarity 42.9%; Pred. No. 2e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TTTGNNNNNNNNCG 14
|||| ||
Db 1 TTTGTCTAGGGCCG 14

RESULT 3
AAZ59895
ID AAZ59895 standard; DNA; 14 BP.
XX
AC AAZ59895;
XX
DT 08-MAY-2000 (first entry)
XX
DE Adenovirus minimal packaging element, A repeat AVI.
XX
KW Adenovirus; minimal packaging element; A repeat; repressor binding site;
KW DNA delivery; ds.
XX
OS Mastadenovirus.
XX
PN WO9953085-A2.
XX
PD 21-OCT-1999.
XX
PF 15-APR-1999; 99WO-US008294.
XX
PR 15-APR-1998; 98US-0081867P.
PR 05-JUN-1998; 98US-0088321P.
XX
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
XX
PI Hearing P, Schmid SI, Ostapchuk PH, Erturk E;
XX
DR WPI; 2000-052657/04.
XX
PT Regulating adenoviral packaging by incorporation of repressor binding
PT sites that allow selective suppression of packaging, used for gene
PT therapy.
XX
PS Disclosure; Page 15; 71pp; English.
XX
CC The invention relates to the regulation of adenoviral packaging. The
CC method of the invention comprises propagating an adenoviral vector
CC containing a repressor binding site, in the absence of the repressor.
CC After propagation, vector packaging is repressed by the appropriate
CC repressor protein. The invention also encompasses an adenoviral vector
CC that includes an adenoviral packaging sequence containing several COUP-TF
CC (chicken ovalbumin upstream promoter transcription factor) binding sites
CC (AAZ59919). Adenoviral vectors containing repressor binding sites are
CC used for DNA delivery, e.g., for expression of a therapeutic protein; in
CC genetic immunisation; or to produce antiviral DNA or antisense RNA.
CC Typical heterologous genes that can be expressed include those for
CC interleukin-2, alpha1-antitrypsin, cystic fibrosis transmembrane
CC conductance regulator and coagulation factor VIII. These vectors have
CC very large capacity (up to 36 kb) for foreign DNA and minimise the risk
CC of generating replication competent virus (since vector and helper virus
CC can be designed such that they have no overlapping packaging sequences

CC that might permit homologous recombination). The presence of the
CC repressor binding site allows selective inhibition of virion production
CC (i.e., packaging of one vector in presence of another). Sequences
CC AAZ59890-Z59896 represent adenovirus minimal packaging elements,
CC designated A repeats AI-AVII, and AAZ59897 represents a consensus of
CC these A repeats
XX
SQ Sequence 14 BP; 2 A; 3 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 42.9%; Score 6; DB 3; Length 14;
Best Local Similarity 42.9%; Pred. No. 2e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TTTGNNNNNNNNCG 14
|||| ||
Db 1 TTTGACCGTTTACG 14

RESULT 4
AAZ59891
ID AAZ59891 standard; DNA; 14 BP.
XX
AC AAZ59891;
XX
DT 08-MAY-2000 (first entry)
XX
DE Adenovirus minimal packaging element, A repeat AII.
XX
KW Adenovirus; minimal packaging element; A repeat; repressor binding site;
KW DNA delivery; ds.
XX
OS Mastadenovirus.
XX
PN WO9953085-A2.
XX
PD 21-OCT-1999.
XX
PF 15-APR-1999; 99WO-US008294.
XX
PR 15-APR-1998; 98US-0081867P.
PR 05-JUN-1998; 98US-0088321P.
XX
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
XX
PI Hearing P, Schmid SI, Ostapchuk PH, Erturk E;
XX
DR WPI; 2000-052657/04.
XX
PT Regulating adenoviral packaging by incorporation of repressor binding
PT sites that allow selective suppression of packaging, used for gene
PT therapy.
XX
PS Disclosure; Page 15; 71pp; English.
XX
CC The invention relates to the regulation of adenoviral packaging. The
CC method of the invention comprises propagating an adenoviral vector
CC containing a repressor binding site, in the absence of the repressor.
CC After propagation, vector packaging is repressed by the appropriate
CC repressor protein. The invention also encompasses an adenoviral vector
CC that includes an adenoviral packaging sequence containing several COUP-TF
CC (chicken ovalbumin upstream promoter transcription factor) binding sites
CC (AAZ59919). Adenoviral vectors containing repressor binding sites are
CC used for DNA delivery, e.g., for expression of a therapeutic protein; in
CC genetic immunisation; or to produce antiviral DNA or antisense RNA.
CC Typical heterologous genes that can be expressed include those for
CC interleukin-2, alpha1-antitrypsin, cystic fibrosis transmembrane
CC conductance regulator and coagulation factor VIII. These vectors have
CC very large capacity (up to 36 kb) for foreign DNA and minimise the risk
CC of generating replication competent virus (since vector and helper virus
CC can be designed such that they have no overlapping packaging sequences
CC that might permit homologous recombination). The presence of the
CC repressor binding site allows selective inhibition of virion production
CC (i.e., packaging of one vector in presence of another). Sequences
CC AAZ59890-Z59896 represent adenovirus minimal packaging elements,
CC designated A repeats AI-AVII, and AAZ59897 represents a consensus of
CC these A repeats
XX
SQ Sequence 14 BP; 1 A; 3 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 42.9%; Score 6; DB 3; Length 14;
Best Local Similarity 42.9%; Pred. No. 2e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TTTGNNNNNNNNCG 14
|||| ||
Db 1 TTTGGCCATTTTCG 14

RESULT 5
AAX64642/c
ID AAX64642 standard; RNA; 15 BP.
XX
AC AAX64642;
XX
DT 20-JUL-1999 (first entry)
XX
DE Human B7-1 hammerhead ribozyme target SEQ ID NO:1274.
XX
KW Arthritic condition; graft tolerance; immune response; target; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9618736-A2.
XX
PD 20-JUN-1996.
XX
PF 22-NOV-1995; 95WO-US015516.
XX
PR 13-DEC-1994; 94US-00354920.
PR 23-DEC-1994; 94US-00363253.
PR 23-DEC-1994; 94US-00363254.
PR 17-FEB-1995; 95US-00390850.
PR 20-APR-1995; 95US-00426124.
PR 02-MAY-1995; 95US-00432874.
PR 04-MAY-1995; 95US-00434509.
PR 07-JUL-1995; 95US-0000951P.
PR 07-JUL-1995; 95US-0000974P.
PR 07-AUG-1995; 95US-00512861.
PR 05-OCT-1995; 95US-00541365.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;
PI Mcswiggen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;
PI Karpeisky A, Thompson JD, Modak A, Burgin A;
XX
DR WPI; 1996-300653/30.
XX
PT Enzymatic nucleic acid molecules having a hammer-head motif - used for
PT the treatment of arthritis, induction of graft tolerance or treatment of
PT auto-immune diseases.
XX
PS Claim 10; Page 167; 307pp; English.
XX
CC The present invention describes a novel enzymatic nucleic acid (ENA)
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues
CC ; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least
CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's
CC can inhibit collagenase and stromelysin production in the synovial
CC membrane of joints for the treatment or prevention of arthritis,
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
CC be used to treat antigen presenting cells of a donor to induce tolerance

CC in a recipient to an alloantigen of a donor. They can also be used for
CC enhancing graft tolerance or for treating autoimmune disease, and for
CC treating allergies and other inflammatory conditions. The ENA's can also
CC be used in diagnosis. Ribozyme therapy impacts on the expression of
CC stromelysin without introducing the non-specific effects upon gene
CC expression which accompany treatment with retinoids and dexamethasone.
CC The concentration of ribozyme required to affect a therapeutic treatment
CC is lower than that required of antisense molecules, and is highly
CC specific. The present sequence is used in the exemplification of the
CC present invention
XX
SQ Sequence 15 BP; 6 A; 3 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 42.9%; Score 6; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 2e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TTTGNNNNNNNNCG 14
|||| ||
Db 15 TTTGACTGATAACG 2

RESULT 6
AAX56323/c
ID AAX56323 standard; DNA; 15 BP.
XX
AC AAX56323;
XX
DT 21-JUL-1999 (first entry)
XX
DE Neisseria gonorrhoeae detection primer GCIR-BL5.1.
XX
KW Neisseria gonorrhoeae; thermophilic strand displacement amplification;
KW homogeneous fluorescent real time tSDA; detection; amplification; primer;
KW tSDA; PCR; 3SR; transcription-mediated amplification; NASBA; ss.
XX
OS Synthetic.
OS Neisseria gonorrhoeae.
XX
PN EP919633-A2.
XX
PD 02-JUN-1999.
XX
PF 03-NOV-1998; 98EP-00120807.
XX
PR 04-NOV-1997; 97US-00963946.
XX
PA (BECT) BECTON DICKINSON & CO.
XX
PI Durmowicz GP, Harris JM, Dilli Yanson K;
XX
DR WPI; 1999-304828/26.
XX
PT New primers specific for Neisseria gonorrhea useful for detecting this
PT bacteria in a sample from a patient.
XX
PS Claim 3; Page 31; 44pp; English.
XX
CC AAX56317 to AAX56355 represent oligonucleotide primers used in the
CC detection of Neisseria gonorrhoeae. The primers may be used to detect the
CC presence of Neisseria gonorrhoeae in a sample from a patient using
CC thermophilic Strand Displacement Amplification (tSDA) or homogeneous
CC fluorescent real time tSDA using dye donor/acceptor pairs. Alternatively
CC they may used as signal primers in other amplification methods such as
CC PCR, 3SR, Transcription-mediated amplification or NASBA. These methods
CC are used to discriminate between the nucleic acids of Neisseria
CC gonorrhoeae and those of other species of bacteria. The oligonucleotides
CC may also be employed before or after culture of Neisseria gonorrhoeae to
CC confirm its identity. Prior art methods of detecting Neisseria
CC gonorrhoeae involved overnight culture of clinical swabs followed by
CC biochemical and/or microscopic identification. The oligonucleotides are
CC designed against sequence- specific regions of Neisseria gonorrhoeae DNA
CC so they can distinguish this species in a sample that may contain other
CC Neisseria species of bacteria. In addition the oligonucleotides and
CC detection kits allow rapid identification of the bacteria without having
CC to resort to the time-consuming prior art methods
XX
SQ Sequence 15 BP; 7 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 42.9%; Score 6; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 2e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TTTGNNNNNNNNCG 14
|||| ||
Db 14 TTTGATGATTTGCG 1

RESULT 7
AAX30272/c
ID AAX30272 standard; DNA; 15 BP.
XX
AC AAX30272;
XX
DT 21-JUN-1999 (first entry)
XX
DE Neisseria gonorrheae target bumper primer GCIR-BL5.1.
XX
KW HIV; gag; bumper primer; amplification primer; probe; detection;
KW fluorescence quenching; Chlamydia trachomatis; Neisseria gonorrheae;
KW human; placental DNA; pathogen; ss.
XX
OS Synthetic.
XX
PN EP915173-A2.
XX
PD 12-MAY-1999.
XX
PF 03-NOV-1998; 98EP-00120832.
XX
PR 04-NOV-1997; 97US-00964020.
XX
PA (BECT) BECTON DICKINSON & CO.
XX
PI Little MC, Vonk GP;
XX
DR WPI; 1999-265943/23.
XX
PT New method for real-time fluorescence-detection assays useful for
PT detecting nucleic acids from pathogens in samples from patients.
XX
PS Example 5; Page 10; 16pp; English.
XX
CC The present invention describes a kit for conducting a fluorescence
CC detection assay to determine the presence, absence or amount of a target
CC analyte in a sample. The method and kit may be used to detect
CC amplification of nucleic acid molecules in real time using fluorescence
CC quenching for example. The assays may be used to detect the presence of
CC nucleic acids from pathogens in samples of body fluid from patients. The
CC kit allows a homogeneous nucleic acid amplification and real time nucleic
CC acid probe detection assay to be carried out with minimal complexity
CC which yields a consistent reliable fluorescent detection signal. The
CC present sequence represents a primer used in the exemplification of the
CC present invention
XX
SQ Sequence 15 BP; 7 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 42.9%; Score 6; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 2e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TTTGNNNNNNNNCG 14
|||| ||
Db 14 TTTGATGATTTGCG 1

```
RESULT 8
AAZ62723/c
ID   AAZ62723 standard; RNA; 15 BP.
XX
AC   AAZ62723;
XX
DT   28-MAR-2000  (first entry)
XX
DE   Substrate for HH ribozyme HCV-6413 which cleaves HCV RNA at nt. 6413.
XX
KW   Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW   cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW   autoimmune disease; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO9955847-A2.
XX
PD   04-NOV-1999.
XX
PF   26-APR-1999;   99WO-US009027.
XX
PR   27-APR-1998;   98US-0083217P.
PR   18-SEP-1998;   98US-0100842P.
PR   25-FEB-1999;   99US-00257608.
PR   23-MAR-1999;   99US-00274553.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts E,  Pavco PA,  Macejak D;
XX
DR   WPI; 2000-062023/05.
XX
PT   Novel ribozymes for the treatment of diseases and conditions related to
PT   hepatitis C infection.
XX
PS   Claim 1; Page 61; 123pp; English.
XX
CC   The present sequence represents the preferred target sequence of an
CC   enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC   the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC   the descriptor line. The HCV sequence was screened for optimal ribozyme
CC   target sites using a computer folding algorithm and regions of the mRNA
CC   which did not form secondary folding structures and contained potential
CC   ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC   target these sites and their activities optimised by either varying the
CC   length of the binding arms or by modification to prevent degradation by
CC   nucleases. The ribozymes of the invention inhibit gene expression and/or
CC   viral replication, and are used to treat diseases associated with
CC   Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC   hepatocellular carcinoma. The ribozymes may be used in combination with
CC   interferon to treat HCV infection, other infectious diseases, autoimmune
CC   diseases, and cancer
XX
SQ   Sequence 15 BP; 6 A; 4 C; 3 G; 0 T; 2 U; 0 Other;

  Query Match             42.9%;  Score 6;  DB 3;  Length 15;
  Best Local Similarity   42.9%;  Pred. No. 2e+05;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||         ||
Db         15 TTTGCATGATGCCG 2


RESULT 9
AAZ59897
ID   AAZ59897 standard; DNA; 15 BP.
XX
AC   AAZ59897;
XX
DT   08-MAY-2000  (first entry)
XX
DE   Consensus adenovirus minimal packaging element (A repeat).
XX
KW   Adenovirus; minimal packaging element; A repeat; repressor binding site;
KW   DNA delivery; ds.
XX
OS   Mastadenovirus.
XX
PN   WO9953085-A2.
XX
PD   21-OCT-1999.
XX
PF   15-APR-1999;   99WO-US008294.
XX
PR   15-APR-1998;   98US-0081867P.
PR   05-JUN-1998;   98US-0088321P.
XX
PA   (UYNY ) UNIV NEW YORK STATE RES FOUND.
XX
PI   Hearing P,  Schmid SI,  Ostapchuk PH,  Erturk E;
XX
DR   WPI; 2000-052657/04.
XX
PT   Regulating adenoviral packaging by incorporation of repressor binding
PT   sites that allow selective suppression of packaging, used for gene
PT   therapy.
XX
PS   Disclosure; Page 15; 71pp; English.
XX
CC   The invention relates to the regulation of adenoviral packaging. The
CC   method of the invention comprises propagating an adenoviral vector
CC   containing a repressor binding site, in the absence of the repressor.
CC   After propagation, vector packaging is repressed by the appropriate
CC   repressor protein. The invention also encompasses an adenoviral vector
CC   that includes an adenoviral packaging sequence containing several COUP-TF
CC   (chicken ovalbumin upstream promoter transcription factor) binding sites
CC   (AAZ59919). Adenoviral vectors containing repressor binding sites are
CC   used for DNA delivery, e.g., for expression of a therapeutic protein; in
CC   genetic immunisation; or to produce antiviral DNA or antisense RNA.
CC   Typical heterologous genes that can be expressed include those for
CC   interleukin-2, alpha1-antitrypsin, cystic fibrosis transmembrane
CC   conductance regulator and coagulation factor VIII. These vectors have
CC   very large capacity (up to 36 kb) for foreign DNA and minimise the risk
CC   of generating replication competent virus (since vector and helper virus
CC   can be designed such that they have no overlapping packaging sequences
CC   that might permit homologous recombination). The presence of the
CC   repressor binding site allows selective inhibition of virion production
CC   (i.e., packaging of one vector in presence of another). Sequences
CC   AAZ59890-Z59896 represent adenovirus minimal packaging elements,
CC   designated A repeats AI-AVII, and AAZ59897 represents a consensus of
CC   these A repeats
XX
SQ   Sequence 15 BP; 1 A; 1 C; 2 G; 3 T; 0 U; 8 Other;

  Query Match             42.9%;  Score 6;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2e+05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||||||||||||
Db          2 TTTGNNNNNNNNCG 15


RESULT 10
AAF46301/c
ID   AAF46301 standard; DNA; 15 BP.
XX
AC   AAF46301;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #1140.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
```

KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 6; Page 41; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 3 A; 9 C; 1 G; 2 T; 0 U; 0 Other;

```
  Query Match           42.9%;  Score 6;  DB 4;  Length 15;
  Best Local Similarity 42.9%;  Pred. No. 2e+05;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         14 TTTGGAGAGGGGCG 1
```

RESULT 11
AAF52545
ID AAF52545 standard; DNA; 15 BP.
XX
AC AAF52545;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #3505.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 8; Page 83; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 3 A; 2 C; 5 G; 5 T; 0 U; 0 Other;

```
  Query Match           42.9%;  Score 6;  DB 4;  Length 15;
  Best Local Similarity 42.9%;  Pred. No. 2e+05;
  Matches    6;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db          1 TTTGGTATGACGCG 14
```

RESULT 12
AAF47804/c
ID AAF47804 standard; DNA; 15 BP.
XX
AC AAF47804;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGFBP3 oligonucleotide #1224.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX

OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 7; Page 52; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 4 A; 5 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 42.9%; Score 6; DB 4; Length 15;
Best Local Similarity 42.9%; Pred. No. 2e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db         15 TTTGATAGGAAGCG 2
```

RESULT 13
AAF49895
ID AAF49895 standard; DNA; 15 BP.
XX
AC AAF49895;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #855.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 8; Page 66; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 1 A; 2 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 42.9%; Score 6; DB 4; Length 15;
Best Local Similarity 42.9%; Pred. No. 2e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db          2 TTTGAGGGCTGGCG 15
```

RESULT 14
AAF52544
ID AAF52544 standard; DNA; 15 BP.
XX
AC AAF52544;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #3504.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX

PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 8; Page 83; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 2 A; 2 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 42.9%; Score 6; DB 4; Length 15;
Best Local Similarity 42.9%; Pred. No. 2e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db          2 TTTGGTATGACGCG 15
```

RESULT 15
AAF52808
ID AAF52808 standard; DNA; 15 BP.
XX
AC AAF52808;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #3768.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 8; Page 85; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 3 A; 2 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 42.9%; Score 6; DB 4; Length 15;
Best Local Similarity 42.9%; Pred. No. 2e+05;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
Qy          1 TTTGNNNNNNNNCG 14
              ||||        ||
Db          2 TTTGAACTGATGCG 15
```

Search completed: April 5, 2004, 06:50:21
Job time : 403 secs